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Probe

Newsletter for the USDA Plant Genome Research Program

Volume 3, No. 1 / 2

January - June 1993

USDA's High-Priority Commitment To the Plant Genome Research Program

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Washington, DC*

The U.S. Department of Agriculture (USDA) is committed to the Plant Genome Research Program. The efficiency and effectiveness of the program during its first 2 years of existence have demonstrated the worthiness of the Department's scientific and financial investments.

The Plant Genome Research Program ranks as one of the most important research program areas in USDA. Achievement of the program's goals will have significant, long-term impacts on improving the quality, productivity, and other characteristics of plants and their products.

The program will provide essential information that will help us keep moving forward with improvements in crops. In some crops, such as corn, soybeans, and wheat, we may be approaching the limits of improvement we can make based on traditional breeding and our current knowledge of the crop.

We must make more rapid progress in adapting major crops and their products to the needs and desires of

both U.S. and foreign processors and consumers. In addition, by the year 2050 the world's population will double, and agriculture will be faced with providing an adequate food supply for an additional 5 billion people, while the land available for agriculture will be decreasing.

Genome map data will allow plant breeders, both traditional and those in molecular biology, to combine their efforts and make more rapid and more predictable progress in their important work. This efficiency can only come as the result of developing a precise description of the gene structure and the traits controlled--information that will reduce the long and difficult task of selective breeding.

We believe that indepth, coordinated research on the genomes of the agronomically important crops is vital to ensuring the future food supply of the United States and the world.

It is especially important that work on plant genomes be a cooperative effort among Federal, university, and industry scientists, fostering an exchange of information and results. Communication and cooperation



are essential. Resources are too tight now to allow for duplicative research--for the wheel to be re-invented again and again.

High-Priority Designation

Research priorities for USDA are the result of a consultative process involving 33 public and private organizations and agencies. Problems and opportunities that should be considered for priority designation are identified by producers, consumers, scientists, educators, and professional societies.

These items are then evaluated and ranked by the Joint Council, in collaboration with the Research and Extension Users Advisory Board, and suggestions for high-priority designation are sent to the Secretary of Agriculture.

In May 1992, 21 areas were assigned a high-priority designation for fiscal year 1993. This list included plant genome mapping and genetic enhancement. "New knowledge about the molecular and cellular processes of animal and plant inheritance is the key to developing new products and to enhancing the safety and nutrition of food," according to the Joint Council report on research priorities.

In addition, results from the Plant Genome Research Program identify genes that control tolerance to an insect pest, then crops with more insect resistance can be developed. With such resistant crops, the need for pesticide application will be reduced, and the possibility of pesticide runoff into ground water will be lessened. Water quality will be easier to maintain or enhance.

Results from the program will also have a ripple effect, helping to improve rural economies as higher value crops with more potential for processing are developed.

USDA Commitment

USDA allocated a budget of \$14.7 million for the Plant Genome Program in fiscal year 1991 and \$15 million in fiscal year 1992; the program was funded at a level of \$18 million for fiscal year 1993.

As an additional sign of USDA's commitment to the Plant Genome Research Program, Dr. Jerome Miksche's appointment as Director of the Plant Genome Research Initiative has been changed from a part-time to a full-time position.

And the National Agricultural Library, with \$2.38 million in interim funding from the Agricultural Research Service, has taken the lead in making the vast amount of information being developed available through computer database systems.

The Plant Genome Research Program has received authorization for 5 years of support. In 1996, at the close of those 5 years, the program will be evaluated and a progress report made to the Secretary of Agriculture and the Congress.

Re-authorization will depend on the program's having achieved tangible results. The Plant Genome Research Program is mission oriented. While basic research is important and technique development is essential, the program must remain focused on economically important traits of crops. Currently, research in this program is addressing agronomic traits in more than 40 crop and tree species.

The impetus for the continuation of the program will come from the successful isolation and transfer of genes that control such traits and their regulatory systems; the development of new gene mapping, sequencing, and automation systems; and the implementation of a national and international database on genetic information.

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The clear exchange of information and the prevention of research duplication will also help ensure the re-authorization of the program. The cooperation of the four USDA agencies directly involved in this program—Agricultural Research Service, Cooperative State Research Service, National Agricultural Library, and Forest Service—has been excellent. Such cooperation must continue and increase.

Cooperation and coordination between this program and the Human Genome Project at the National Institutes of Health and the Department of Energy have also enhanced the productivity and

efficiency of both projects. There has been a practical interchange of information on new technologies and basic genomic research data.

In the short time—just 2 years—that the NRI Plant Genome Competitive Grants Program has been under way, the identification and mapping of some insect and plant disease resistance gene systems are already nearing the point where they can be tested by breeders.

This bodes well for the effectiveness of a targeted competitive grants approach to solving difficult, critical agricultural problems. ♦

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ASCB Newsletter **A Special Education Issue**

The July 1993 issue of the ASCB Newsletter will be devoted to educational activities of the American Society for Cell Biology.

This issue will include special features on:

- ☐ A new ASCB Cell Biology teaching video that will be featured at the 1993 Annual Meeting.
- ☐ Examples of local educational programs throughout the country.
- ☐ The Coffee Break Forums during the ASCB Annual Meeting.
- ☐ CELS and AAAS Symposia.
- ☐ The ASCB Summer Teacher Fellowship Program.
- ☐ Details about the new Education and Minority Affairs Committees exhibit booth at the ASCB 1993 Annual Meeting in New Orleans, December 11-15, 1993.

For more information on how to obtain this ASCB Newsletter, write to the American Society for Cell Biology, 9650 Rockville Pike, Bethesda, Maryland. 20814-3992

Touching Base with David Neale



Progress Reported at Forest Tree Genome Mapping Workshop

Dr. David B. Neale, Molecular Geneticist
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Forest trees present many unique and interesting challenges for researchers constructing genetic maps. For example, in forest trees, inbreeding is generally not possible, multigeneration pedigrees are rare, generation times are long, genome sizes are large, and resources are limited.

Recently forest tree genome researchers met to discuss approaches to mapping in trees and to report on the progress of various mapping projects. The meeting was the first Forest Tree Genome Mapping Workshop, one segment of the Plant Genome I Conference held in San Diego, CA. Approximately 80 persons attended the workshop, organized by David Neale (Institute of Forest Genetics, Albany, CA). Fourteen invited speakers participated.

Progress Reports

The workshop opened with a progress report by Toby Bradshaw (University of Washington) on the mapping of *Populus* (*P. trichocarpa* x *P. deltoides*). The map will be used to identify quantitative trait loci (QTL)

influencing growth and form characteristics. Bradshaw noted that severe segregation distortion was observed at one locus, which was attributed to a recessive lethal allele in the *P. trichocarpa* female parent.

Dario Grattapaglia (North Carolina State University, presented by Ron Sederoff) reported on a 548 RAPD marker map in hybrid *Eucalyptus* (*E. grandis* x *E. urophylla*) based on a pseudo-testcross mapping strategy. This approach avoids the loss of information associated with dominant markers in diploid mapping populations. Andrew Groover (Institute of Forest Genetics) presented preliminary results on the mapping of QTLs influencing wood specific gravity in a 3-generation loblolly pine (*Pinus taeda*) pedigree.

In another presentation, John Carlson (University of British Columbia) reported on RAPD mapping in white spruce (*Picea glauca*) and localization of rDNA loci using fluorescence in situ hybridization (FISH). Michael Devey (Institute of Forest Genetics and CSIRO) reported on a novel method to map a dominant gene for resistance to white pine

blister rust (*Cronartium ribicola*) in sugar pine (*Pinus lambertiana*). His strategy employed bulked segregation analysis of haploid megagametophytes from a mother tree heterozygous for the dominant resistance gene. Ten RAPD markers were very closely linked to the resistance gene.

In addition, Keith Hutchison (University of Maine) described the method of single-stranded conformational polymorphism of RAPD fragments to reveal codominant markers in larch and a method to detect variation by PCR from single pollen grains. Warren Nance (Forest Service) reported on the construction of RAPD maps in slash pine (*Pinus eliottii*) and automation technology for large-scale mapping projects. David O'Malley (North Carolina State University) presented a RAPD map for loblolly pine based on haploid segregations from a single mother tree. A method to map QTLs in open-pollinated families was also presented. Dave Harry (Institute of Forest Genetics) described approaches to developing codominant PCR-based markers for trees to avoid the limitations imposed by RFLPs and RAPDs. Gavin Moran (CSIRO) reported on mapping in Monterey pine (*Pinus radiata*) and *Eucalyptus nitens* in Australia.

Statistical Problems

The second part of the workshop addressed statistical problems specifically related to linkage mapping, QTL mapping, and marker breeding in forest trees.

Steve Knapp (Oregon State University) discussed linkage mapping in outbreeding populations; Tom Mitchell-Olds (University of Montana) addressed similar issues related to QTL mapping. Claire Williams (Weyerhaeuser Company) described how molecular marker information might be incorporated into a loblolly pine breeding program.

Database Development

The last part of the workshop focused on the development of a genome database for forest trees. Brad Sherman (Institute of Forest Genetics) presented an on-line demonstration of APtDB, a *Pinus taeda* database. He showed how forest tree genome researchers could contribute data to the database and how users could access it through the Internet.

1994 Workshop

Plans are under way to hold a second workshop at the Plant Genome II meeting in early 1994. Low-density maps have just been completed for a few of the major species. It is expected that by the next meeting many more maps will have been completed, QTLs for important traits will have been identified, and numerous other applications of molecular markers and maps will be commonplace in forest genetics research. ♦

In Memoriam, Dr. Robert Warmbrodt



Photo by Joseph Swab

On December 15, 1992, the National Agricultural Library (NAL) regrettably learned of the death of Dr. Robert Warmbrodt, who had been coordinator of the NAL's Biotechnology Information Center since December 17, 1990. Dr. Warmbrodt, 45, died of AIDS-related complications. Memorial services and interment were held by his family in Missouri.

Dr. Warmbrodt had been a plant physiologist with 20 years of professional experience prior to joining the staff of NAL. He had conducted laboratory research in the Climate Stress and the Plant Physiology

Laboratories at the Agricultural Research Service, Beltsville Agricultural Research Center, from 1978 to 1990. His primary interests concerned the cellular and molecular aspects of photosynthate partitioning.

A native of Boonville, Missouri, Dr. Warmbrodt had an A.B. degree in botany and chemistry from the University of Missouri-Columbia, and a master's degree in botany and a Ph.D. in botany and horticulture, both from the University of Wisconsin-Madison. He also was an Alexander von Humboldt Fellow at the University of Göttingen in Göttingen, Germany.

Dr. Warmbrodt's other work experience included research in horticulture at the University of Maryland-College Park and in botany at the University of Wisconsin-Madison; teaching assignments in botany at Ohio State University-Columbus and the University of Wisconsin-Madison; and a year collecting plants in Panama and Costa Rica for the Missouri Botanical Gardens.

As Coordinator of the Biotechnology Information Center, Dr. Warmbrodt managed the acquisition, compilation, and dissemination of information on the impact of the science of biotechnology on agriculture in the United States and the world. He was concerned with all aspects of agricultural biotechnology as well as the theory and techniques of genetic engineering, plant and animal tissue culture, risk assessment of the release of genetically engineered organisms, and regulation of the field of biotechnology. He authored and co-authored numerous NAL publications, particularly in the two series *Quick Bibliographies* and *Bibliographies and Literature of Agriculture*. - Joseph Swab

The Newsletter "Rice Genome"

The third issue of the newsletter "Rice Genome" (Volume 2, No. 1, July 1993) contains articles on the following topics:

- Multigene families discovered by large scale cDNA analysis
- A high-density STS and EST linkage map of rice
- The rice RFLP linkage map
- SSCP analysis of rice genome DNA
- Construction of YAC contigs
- Use of cosmid libraries for physical mapping
- DNASIS automatic analysis system
- and many smaller interesting feature articles.

The newsletter is available free of charge. To have your name added to the mailing list, send your name and address to the address below. Please indicate also the source of this announcement.

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The next issue of the newsletter will be published by the end of 1993. We cordially invite contributions (news items, short articles, announcements etc.) from the international plant genome research community. DEADLINE for manuscripts is October 1, 1993.

BEYOND DNA PROBES

We invite you to attend the Eighth Annual San Diego Conference on Nucleic Acids featuring scientists from industry, health care and academia; sharing their latest discoveries and advances.

1993 San Diego Conference

This year's program will feature:

November 18, 19, 20

Gene Discovery

Patentability of Genes

Gene Therapy and Antisense

Newly Discovered Properties
of Nucleic Acids

Diagnostics and Clinical Lab Entry

Emerging Technologies

and Applications

Hyatt Regency San Diego

Co-Sponsored By: The San Diego Section A.A.C.C.,
The American Association for Clinical Chemistry, Inc.
and the A.A.C.C. Molecular Pathology Division

For further information contact: Scherago International, Inc. 11 Penn Plaza, Suite 1003, New York, NY 10001 Telephone: (212) 643-1750 Fax: (212) 643-1758

Other Pursuits



China's Rice Genome Research Program

Guofan Hong, Head

Rice Genome Research Program, Shanghai Institute of Biochemistry
Academia Sinica, Shanghai, China

The Chinese Rice Genome Research Program (RGP) is one effort initiated to help modernize China's agriculture. China possesses the largest rice-producing land area in the world--rice output accounts for about half of the country's total grain yield.

China has a long history in rice cultivation and accumulated experiences in breeding. The results obtained from RGP will be applied to plant breeding. New concepts derived from the research should prove useful in improving one's

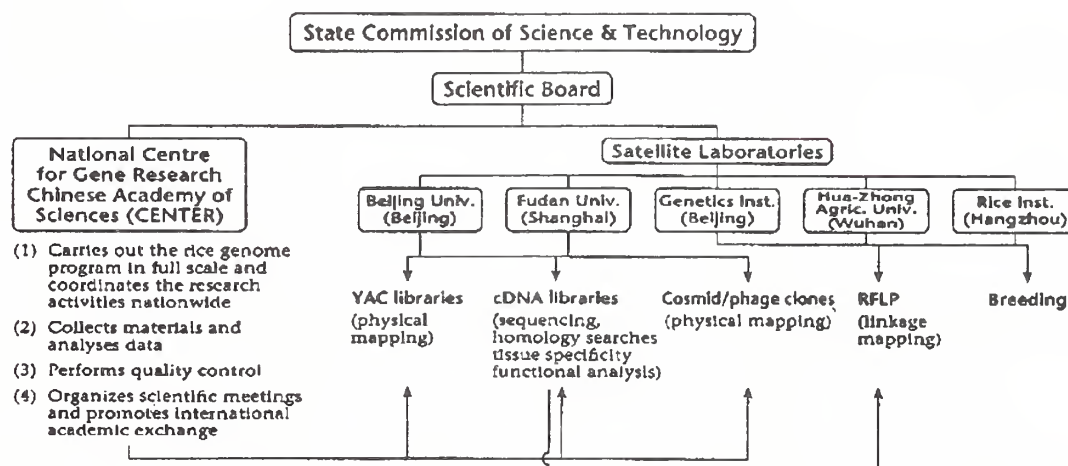
understanding of the plant life phenomena as a whole.

Research Areas

The mapping and sequencing of the entire rice genome is expected to be completed in about 15 years, so that the complex genetic machinery of the entire genome would be elucidated at the DNA level.

The extent to which the DNA sequences will be determined will depend on the degree of development in related fields of technology. Currently research is focused on the following:

- (1) Isolating, characterizing, and sequencing genes of biological importance;
- (2) Characterizing and mapping agronomically important genes, and applying the results to breeding when possible;
- (3) Constructing an ordered set of genomic DNA clones, used to construct physical and genetic maps of the chromosomes;
- (4) Elucidating the mechanisms for coordinated and programmed gene expression; and
- (5) Establishing an internationally connected computer center.



Organizational chart is reprinted with permission from the Rice Genome Newsletter, Volume 1, Number 2. (1993)

Gene Research Center

Under the State Commission of Science and Technology (SCST) the scientific board that directs RGP was established. Consigned by SCST, the Chinese Academy of Sciences will establish a National Center for Gene Research (NCGR) in Shanghai. NCGR's primary responsibilities will be as follows:

- (1) Carrying out the RGP in full scale, and coordinating research activities nationwide;
- (2) Collecting materials and analyzing data;
- (3) Providing quality control; and
- (4) Organizing scientific meetings and promoting international academic exchange.

Satellite Laboratories

In addition to NCGR, five satellite laboratories will be assigned research tasks based on their respective expertise. These laboratories are located in the Institute of Genetics, the Chinese Academy of Sciences; Beijing University; Hua-Zhong Agricultural University; Fudan University; and the National Rice Institute.

Funding

Approximately \$4 million (23 million yuan) has been allocated by the Chinese government to support the program for the first 5 years. During this period, some adjustments may be

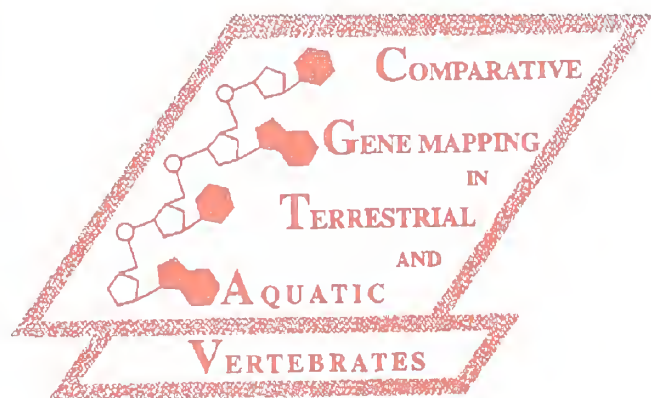
made to meet new development requirements.

Collaborative Effort

Participants in RGP anticipate international collaboration and hope to share their research results with interested scientists worldwide.

For more information, contact the Shanghai Institute of Biochemistry, Academia Sinica, 320 Yue-Yang Road, Shanghai, 200031 China.

Phone: +86-21-4374430; FAX +86-21-4338357.◆



Tentative Program:

- Advanced Technologies for Comparative Gene Mapping
- Comparative Mapping and Genome Evolution
- Genome Diversity and Function
- Disease Genetics
- Applications to Agriculture and Medicine

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Where: Oslo Norway

When: February 7-11, 1994

Attendance will be limited to approximately 150 participants

Supergene™ Software Assists DNA Marker Analysis Via Graphical Display

Drs. Sam Boutin and Nevin Young, Department of Plant Pathology, University of Minnesota, Minneapolis; and Dr. Randy Shoemaker, USDA, Agricultural Research Service, Department of Agronomy, and Dr. Lisa Lorenzen, Department of Zoology and Genetics, Iowa State University, Ames

Genomic analysis based on DNA genetic markers leads to vast amounts of information. This information can be stored in various ways, including spreadsheets and databases, and presented in a multitude of different text or graphical displays.

Graphical display allows for rapid visualization of data and can potentially simplify interpretation. One example is the display of linkage maps and pedigrees derived from DNA marker studies in a color graphic format. Such graphical images give a powerful visual overview of the genetic relationships between individuals in a single population or between varieties in a species.

Supergene™

A recently developed computer software package, Supergene™, was developed to assist in DNA marker analysis using graphical display. Supergene™ converts DNA marker data into a color graphic format and

gives the user the ability to (1) draw a graphical genotype for a selected individual, (2) draw a single linkage group for many selected individuals, and (3) draw a DNA-based pedigree to or from a genotype.

Supergene™ enables genetic comparisons on a macro level by comparing whole genomes, as well as more focused comparisons, such as linkage groups. In a graphical genotype, each portion of the genome

such as those that may carry desirable genes, can be highlighted in the graphical genome representations. This should be helpful in breeding programs for selecting individuals based on genotype and in monitoring the DNA genotypes of progeny individuals.

Using Supergene™

Supergene™ can be used in the analysis and comparison of any type of genome. For studies in plants, it has been used to detect differences and similarities in the genomes of various cultivars, plant introductions, and their progeny. Supergene™ allows the user to list various genotypes, their parents, their loci, map location, and their DNA marker scores in a table. The user can then view a graphical representation

of an individual's genome, a side-by-side linkage

group comparison between individuals or varieties, and graphical displays of the pedigree for a single linkage group or entire genome.

Developments

is drawn to scale based on genetic distance between markers. The region around each marker is colorized according to the DNA genotype. Finally, for DNA marker-based pedigrees, a graphical image for each linkage group (or genome) is simultaneously displayed for a selected individual, its parents, and grandparents.

Interesting genomic regions,

What You See

Data Table

When Supergene™ is first started, a data table containing individual names, DNA marker names, DNA

Figure 1.

Genotype	Parent 1	Parent 2	A487	B030	A170	K636	A085	T153a	A505	T036	A333
Mandarin			1	1.0488	1.101	1.1618	1.1848	1.2291	1.3488	1.3593	2
Manchu			2	1	0	1	2	1	2	1	1
MandOtt			2	1	1	1	2	1	2	1	1
Richland			1	1	0	1	1	1	0	2	1
AKHarrow			1	2	1	1	1	1	1	1	1
Mukden			1	1	0	2	2	1	2	1	1
Illini			1	2	1	1	1	1	1	2	1
Dunfield			1	2	2	1	2	1	1	1	1
ONS			1	1	1	1	1	1	1	1	1
ManitobaBr			1	1	1	1	2	1	2	0	1
Tokyo			1	1	1	1	1	1	1	2	1
PI54610-4			1	1	1	2	2	2	2	0	1
S100			1	2	1	0	1	1	1	1	0
Pagoda	ManitobaBr	Mandarin	1	1	1	1	2	1	2	1	1
Acme			1	1	1	1	2	1	2	1	1
Lincoln	Mandarin	Manchu	2	2	1	1	1	1	1	1	1
Capital	St. 171	AKHarrow	2	2	1	1	1	1	1	1	1
Hawkeye	Mukden	Richland	1	1	1	2	2	1	2	1	1
BlackHawk	Mukden	Richland	1	1	1	2	2	1	1	2	1
Evans	Merit	Harosoy	1	1	1	1	1	1	1	2	1
McCall	Z	Hark	1	1	1	1	2	1	2	1	1
Harosoy 63			1	1	1	1	2	1	2	1	1
Lee	S100	ONS	1	2	1	1	1	1	1	1	1
Clerk 63			2	2	1	1	1	1	1	1	1
Century	Calland	Bonus	2	1	2	1	2	1	2	1	1
Chippewa	Lincoln	Richland	2	2	1	1	1	1	1	2	1
Ford	Lincoln	Richland	2	1	1	1	1	1	1	1	1
Shelby	Lincoln	Richland	0	2	1	1	1	1	1	2	1
Merit	BlackHawk	Capital	1	2	1	1	1	1	1	2	1
Kent	Lincoln	Opden	2	2	2	1	2	1	1	1	1
Adelphi	Kent	Adams	2	2	2	1	2	1	1	1	1

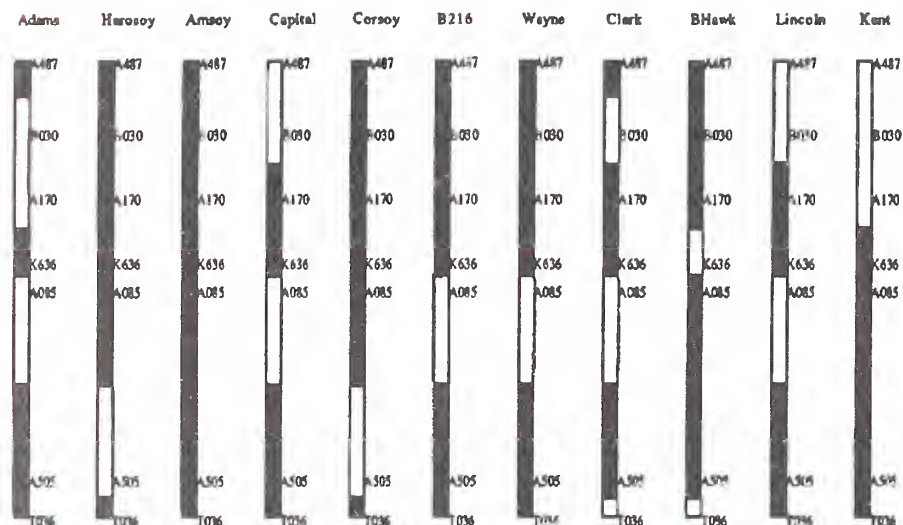
marker loci, parent names, and numerical genotype scores is displayed on the screen. This information can be entered manually, but would be imported from a spreadsheet program. Figure 1 illustrates a typical data table.

The first column of the table contains the genotypes, the second and third columns contain the names of parent lines, and the remaining columns contain the scores for the genetic markers. The name for each marker and its map location are located at the top of these columns. Presently, the table handles up to 200 markers and 335 individuals.

Genetic marker data identifies the genetic constitution of the genomes at a particular locus. If the genomes of the two different individuals are the same at a locus, the score is the same. When the genomes differ at the same locus, the scores differ. With the types of DNA mark-

ers currently in use (RFLP and RAPDs), only two alternate alleles are often observed at each locus for inbred crop species. Improved and more polymorphic DNA markers are likely to show several alleles available at a single locus. Supergene™ can handle several alleles at the same locus through the use of different colors.

Figure 2.



The user can then display the desired graphic via the Graphics menu. These displays include the entire genome, single linkage group comparison (fig. 2), linkage group pedigree (fig. 3), and genome pedigree.

Genome Display

The Create Map command illustrates all the linkage groups of an individual genome with their loci colored according to their numerical genotype score. After the individual's name is entered, the software draws each linkage group, labels the loci, and colorizes the loci according to the score.

Single Linkage Group Display

Often a side-by-side comparison of the same linkage group from different individuals is desired (fig. 2). When the Single Linkage Group command in the Graphics menu is selected, the user is prompted for the linkage group number to be drawn. The software draws the same linkage group for all individuals listed in the table. The same locus on the same

linkage group among different individuals can be compared by color.

Linkage Pedigree Display

A comparison of the same linkage group among ancestors of a particular individual is often desired (fig. 3). The Linkage Pedigree command under the Graphics menu prompts the user for an individual name. The software draws the pedigree for the individual, the parents, and grandparents that reside in the table. The same locus on the same linkage group from different ancestors can be compared, since each allele is a different color. The inheritance of that locus through the pedigree can be followed.

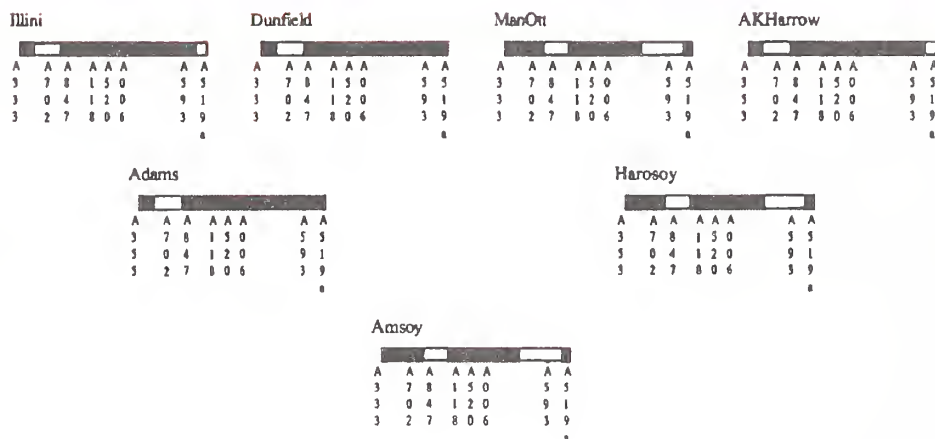
Genome Pedigree Display

If a macroscopic comparison of all the genomes in a pedigree is desired, the Genome Pedigree command can be used. The user is again prompted for the individual; the software then draws out the genome for that desired individual, its parents, and grandparents in a pedigree format. All the linkage groups for each individual in the pedigree can then be compared.

Macro and Micro Views

Since both macro and micro views of the genome and linkage groups are of interest, Supergene™ allows for scaling the various graphics. The user has the option of selecting a scaling factor. This allows for squeezing as much into the display as possible or expanding the view so that markers only a few centimorgans apart can be resolved.

Figure 3.



What Supergene™ Isn't

The purpose of Supergene™ is to transform data into useful graphical images rendering genetic information. The software does not have sophisticated graphics or spreadsheet capability. However, many packages are available on the market for users who desire additional manipulation of the graphics or data.

The data should be manipulated in a spreadsheet prior to importing it into Supergene™; additional detail should be added to the graphics by copying the drawings and pasting them into a graphics application. Significantly, the graphics output are "draw" objects (as opposed to "paint" or bit-mapped graphic), so each component of a graphical image can be manipulated individually by a suitable computer software application.

Computer Environment

Supergene™ is a stand-alone application written in Supertalk™, a scripting language of Aldus Supercard. Supergene™ runs on all Macintosh II family computers. However, convert-

ing numerical data into graphical images requires considerable processing, so the higher end of the line is strongly recommended. A color display is obviously preferred, but the software draws different patterns for black and white models.

Support

Supergene™ was supported by a specific cooperative agreement for the USDA, Agricultural Research Service Plant Genome Database Program. This paper is a contribution of the Minnesota Agricultural Experiment Station series on research conducted under Project 015, supported by GAR funds.

Contact

Readers who desire additional information should contact Sam Boutin via Internet at boutin@molbio.cbs.umn.edu or via FAX (612) 625-9728. ♦

Mention of a trade name or brand does not constitute endorsement or recommendation by the Department over similar products not named.

Off the Wire

New Service From National Center for Biotechnology Information

Dennis Benson

National Center for Biotechnology Information

National Library of Medicine

Bethesda, MD

The National Center for Biotechnology Information (NCBI), National Library of Medicine, now provides e-mail server access for sequence similarity searching (BLAST) and for record retrieval from sequence databases.

The BLAST e-mail server accepts either a DNA or amino acid query sequence in FASTA format, runs the search against a combined (non-redundant) or a single database, and returns the results in a mail message.

The RETRIEVE e-mail server accepts single or multiple text strings (locus names, accession numbers, keywords, author names, etc.) as queries; runs an IRX search against a specified database; and returns the matching full record(s) as a mail message.

To receive documentation on how to use the servers, send a mail message with the word "help" in the body of the message to:

BLAST server: blast@ncbi.nlm.nih.gov

RETRIEVE server: retrieve@ncbi.nlm.nih.gov

The following BLAST databases are available:

Peptide Sequence Databases

Name	Description
nr	Non-redundant protein database (selected automatically by blastp; includes SWISS-PROT, PIR, GenPept, and GenPept updates)
swissprot	SWISS-PROT protein database
pir	PIR protein database
genpept	GenPept (translated GenBank)
gpupdate	GenPept update (cumulative daily updates)

tfd Transcription Factors Database

Nucleotide Sequence Databases

Name	Description
nr	Non-redundant DNA database (selected automatically by blastn; includes GenBank, GenBank updates, EMBL, and EMBL updates)
genbank	GenBank DNA sequence database (does not include updates)
gbupdate	GenBank update (cumulative daily updates)
embl	EMBL DNA sequence database (does not include updates)
emblu	EMBL update (cumulative weekly updates)
vector	Vector subset of GenBank (LANL)
dbest	Database of Expressed Sequence Tags (ESTs)

Additional Assistance

For additional general information, send e-mail to: info@ncbi.nih.gov. For specific information on the operation of the servers, not covered in the documentation, send e-mail to: blast-help@ncbi.nlm.nih.gov or retrieve-help@ncbi.nlm.nih.gov.

Readers may also write to Dennis Benson at the National Center for Biotechnology Information, National Library of Medicine, Bethesda, MD 20894 or contact him by phone on (301) 496-2475 or by e-mail: benson@ncbi.nlm.nih.gov. ♦

On the Horizon



Calendar of Upcoming Genome Events

Meetings

July 31-August 4: **DNA Damage - Effects on DNA Structure and Protein Recognition**, Burlington, VT. Contact: New York Academy of Sciences, Conference Dept., 2 East St., New York, NY 10021. Telephone: (212) 838-0230, FAX: (212) 838-5640.

July 31-August 4: **1993 Joint Meeting of The American and Canadian Societies of Plant Physiologists**, Minneapolis, MN. Contact: Dorothy Croft, American Society of Plant Physiologists, 15501 Monona Dr., Rockville, MD 20855-2768. Telephone: (301) 251-0560, FAX: (301) 279-2996.

August 1-6: **Photosynthesis: Biochemical Aspects of**, New Hampton, NH. Contact: Dr. Alexander M. Cruickshank, Director, Gordon Research Conferences, Colby-Sawyer College, New London, NH 03257. Telephone: (603) 526-2870, FAX: (603) 526-4717.

August 2-4: **44th American Institute of Biological Sciences Annual Meeting**, Ames, IA. Contact: AIBS, 730 11th Street NW, Washington, DC 20001-4521. Telephone: (202) 628-1500, FAX: (202) 628-1509.

August 2-7: **4th Gordon Research Conference on Quantitative Genetics and Biotechnology**, Ventura, CA. Contact: University of Minnesota, Dr. F. Enfield, Dept. of Genetics and Cell Biology, St. Paul, MN 55108.

August 4-6: **1st International Symposium on Plant Dormancy**, Corvallis, OR. Contact: Dr. G. Lang, Symposium Convenor, 137 Julian C. Miller Hall, Louisiana State University, Baton Rouge, LA 70803-2120. Telephone: (504) 388-1043, FAX: (504) 388-1068.

August 6-10: **Science Innovation '93: New Techniques in Biomolecular Research**, Boston, MA. Contact: AAAS Meetings Office, 1333 H St., NW, Washington, DC 20005. Telephone: (202) 326-6450, FAX: (202) 289-4021.

August 6-9: **Plant Growth Regulator Society of America 20th Annual Meeting**, St. Louis, MO. Contact: Dr. L. Ferguson, Program Chair, University of California, Kearny Agricultural Research Center, 9240 S. Riverbend Ave., Parlier, CA 93648. Telephone: (209) 891-2500.

August 15-21: **17th International Congress of Genetics, Genetics and the Understanding of Life**, Birmingham, UK. Contact: Congressional Secretariat Derek Smith, Research Support and Industrial Liaison, The University of Birmingham, Edgbaston, Birmingham B15 2TT, UK. Telephone: (021) 414-5888, FAX (021) 414-3850.

August 19-22: **ARABIFLORA: The 5th International Conference on Arabidopsis Research**, Ohio State University, Columbus, OH. Contact: Arabidopsis Conference, Conference Unit, The Ohio State University, 225 Mount Hall, 1050 Carmack Rd., Columbus, OH 43210-1002. Telephone: (614) 292-8571, FAX: (614) 292-0492.

September 6-10: **Sixth International Conference on Applied Algology**, Trebon, Slovak Republic. Contact: Institute of Microbiology, Jiri Doucha, Dept. of Autotrophic Microorganisms, 37981 Trebon, Slovak Republic. Telephone: 42-333-2421, FAX: 42-333-2268.

September 9-10: **Down Regulation of Gene Expression by Antisense and Other Technologies Symposium**, Ames, IA. Contact: Dr. Cecil Stewart, Dept. of Botany, Iowa State University, Ames, IA 50011. Telephone (515) 294-1063, FAX: (515) 294-1337, EMAIL: sl.sto@isumvs.iastate.edu.

September 12-16: **Symposium on Improvement of Cereal Quality by Genetic Engineering: 43rd Australian Cereal Chemistry Conference**, Coogee Beach, Sydney, Australia. Contact: Dr. R. Henry, Vice-Chairman Cereal Chemistry Division RACI, Queensland Agricultural Biotechnology Centre, Gehrman Laboratories, University of Queensland 4067. Telephone: (07) 3654962; FAX: (07) 3654980.

September 13-17: **24th Annual Meeting of the European Society for New Methods in Agricultural Research**, Leipzig, Germany. Contact: Wye College, Prof. D.A. Baker, Dept. of Biochemistry, Ashford, Kent TN25 5AH, UK.

September 19-22: **2nd National Symposium on PLANAR CHROMATOGRAPHY: Modern Thin-Layer Chromatography**, Research Triangle Park, NC. Contact: Planar Chromatography Symposium Manager, Mrs. Janet Cunningham, Barr Enterprises, P.O. Box 279, Walkersville, MD 21793. Telephone: (301) 898-3772, FAX: (301) 898-5596.

September 27-October 1: **DNA Repair and DNA Replication Strategies**, St. Johns College, Cambridge, UK. Contact: Dr. R.T. Johnson, Dept. of Zoology, Downing St., Cambridge CB2 3EJ, UK.

October 10-15: **Photosynthetic CO₂ Fixation and Metabolism in Plants**, Irsee, Germany. Contact: Dr. Alexander M. Cruickshank, Director, Gordon Research Conferences, Colby-Sawyer College, New London, NH 03257. Telephone: (603) 526-2870, FAX: (603) 526-4717.

October 11-12: **International Conference on Strategic Business Information in Biotechnology**, Research Triangle Park, NC. Contact: Institute for Biotechnology Information, North Carolina Biotechnology Center, P.O. Box 13547, Research Triangle Park, NC 27514-3547. Telephone: (919) 549-8880, FAX: (919) 990-952

October 13-16: **DNA: The Double Helix - Forty Years: Perspective and Prospective**, Chicago, IL. Contact: New York Academy of Sciences, Conference Dept., 2 East 63rd St., New York, NY 10021. Telephone: (212) 838-0230, FAX: (212) 838-5640.

October 23-27: **Genome Sequencing and Analysis Conference V**, Hilton Head Island, SC. Contact: Susan Wallace, 932 Clopper Rd., Gaithersburg, MD 20878. Telephone: (301) 216-9567, FAX: (301) 977-7233, EMAIL: TIGR (swallace@bengal.tigr.org).

November 7-10: **Electrophoresis '93**, Charleston, SC. Contact: Janet Cunningham, Symposium Manager, c/o The Electrophoresis Society, P.O. Box 279, Walkersville, MD 21793. Telephone: (301) 898-3772, FAX: (301) 898-5596.

November 18-20: **Beyond DNA Probes**, San Diego, CA. Contact: Scherago International, Inc., 11 Penn Plaza, Suite 1003, New York, NY 10001. Telephone: (212) 643-1750.

December 11-15: **Thirty-Third Annual Meeting**, New Orleans, LA. Contact: The American Society for Cell Biology, 9650 Rockville Pike, Bethesda, MD 20814-3992. Telephone: (301) 530-7153. Fax: (301) 530-7139.

WORKSHOPS AND COURSES

August 1-7: **Wheat Genome Mapping Workshop**, Cornell University, Ithaca, NY. Contact: ITMI Wheat Genome Mapping Workshop, Cornell University Conference Services, Box 3 - Robert Purcell Union, Ithaca, NY 14853. Telephone (607) 255-6290.

August 17-20: **Plant Biotechnology Methods**, University Park, PA. Contact: Patricia Phillips, Program Coordinator, Penn State Biotechnology Institute, Pennsylvania State University, 519 Wartik Laboratory, University Park, PA 16802-5807. Telephone: 1-800-833-5533, FAX: (814) 863-1357.

September 6-17: **Techniques in Molecular Biology - Introductory Workshops in Proteins Nucleic Acids and Microbiology**, Hatfield, UK. Contact: University of Hertfordshire, Science Training Centre, College Lane, Hatfield, AL10 9AB, UK. Telephone: (0707) 284 590; FAX: (0707) 284 514.

October 11-14: **Recombinant DNA Methodology**, Lake Tahoe, NV. Contact: Director, Center for Advanced Training in Cell and Molecular Biology, 103 McCort-Ward Bldg., The Catholic University of America, Washington, DC 20064. Telephone: (202) 319-6161, FAX: (202) 319-4467 and (202) 319-5721.

October 11-14: **DNA Sequencing**, Lake Tahoe, NV. Contact: Director, Center for Advanced Training in Cell and Molecular Biology, 103 McCort-Ward Bldg., The Catholic University of America, Washington, DC 20064. Telephone: (202) 319-6161, FAX: (202) 319-4467 and (202) 319-5721.

October 11-14: **PCR Techniques**, Lake Tahoe, NV. Contact: Director, Center for Advanced Training in Cell and Molecular Biology, 103 McCort-Ward Bldg., The Catholic University of America, Washington, DC 20064. Telephone: (202) 319-6161, FAX: (202) 319-4467 and (202) 319-5721.

October 12-15: **DNA Fingerprinting**, Rockville, MD. Contact: American Type Culture Collection, 12301 Parklawn Dr., Rockville, MD 20852-1776. Telephone: (301) 881-2600, FAX: (301) 231-5826.

November 2-5: **Polymerase Chain Reaction/Cycle DNA Sequencing**, Rockville, MD. Contact: American Type Culture Collection, 12301 Parklawn Dr., Rockville, MD 20852-1776. Telephone: (301) 881-2600, FAX: 231-5826.

FUTURE EVENTS

January 24-27, 1994: **Plant Genome II**, San Diego, CA. Contact: Scherago International, 11 Penn Plaza, Suite 1003, New York, NY 10001. Telephone: (212) 643-1750, FAX: (212) 643-1758.

February 7-11, 1994: **Comparative Gene Mapping in Terrestrial and Aquatic Vertebrates**, Oslo, Norway. Contact: Harris A. Lewin, Dept. of Animal Sciences, University of Illinois, 206 Plant & Animal Biotechnology Laboratory, 1201 W. Gregory Drive, Urbana, IL 61801. Telephone: (217) 333-5998; FAX: (217) 244-5617; BITNET: BLOOD@UIUCVMD.

May 8-13, 1994: **HPLC '94, 18th International Symposium on High Performance Liquid Chromatography**, Minneapolis, MN. Contact: Barr Enterprises, P.O. Box 279, Walkersville, MD. Telephone: (301) 898-3772, FAX: (301) 898-5596.

June 19-24, 1994: **4th International Congress of Plant Molecular Biology**, Amsterdam, The Netherlands. Contact: Congress Secretariat, c/o RAI Organisatie Bureau Amsterdam bv, Europaplein 12, 1078 GZ Amsterdam, The Netherlands. Telephone: +31 (0)20 549 1212, FAX: +31 (0)20 646 4469, Telex: 13499 raico nl.

July 17-24, 1994: **5th International Symposium on Genetics and Molecular Biology of Plant Nutrition**, University of California, Davis, CA. Contact: D.W. Rains, Dept. of Agronomy and Range Science, University of California, Davis, CA 95616-8515. Telephone: (916) 752-1711, FAX: (916) 752-4361.

August 4-6, 1994: **1st International Symposium on Plant Dormancy**, Corvallis, OR. Contact: Dr. G. Lang, Symposium Convenor, 137 Julian C. Miller Hall, Louisiana State

University, Baton Rouge, LA 70803-2120. Telephone: (504) 388-1043, FAX: (504) 388-1068.

August 4-6, 1994: **Plant Growth Regulator Society of America 21st Annual Meeting**, Portland, OR. Contact: Dr. L. Ferguson, Program Chair, University of California, Kearny Agricultural Research Center, 9240 S. Riverbend Ave., Parlier, CA 93648. Telephone: (209) 891-2500.

June 16-21, 1996: **HPLC '96, 20th International Symposium on High Performance Liquid Chromatography**, San Francisco, CA. Contact: Barr Enterprises, P.O. Box 279, Walkersville, MD. Telephone: (301) 898-3772, FAX: (301) 898-5596.

IMPORTANT

Plant Genome Grant Deadline Pushed Up

Please note that the deadline for submitting 1994 Plant Genome grant proposals may be several weeks earlier this year; even as early as **November**. We ask that you share this information with interested colleagues.

For more information contact:

Dr. Ed Kaleikau
NRICG/CSRS/USDA
Rm. 323 Aerospace Bldg.
901 D. St., SW
Washington, DC 20250-2241.
Telephone: (202) 401-5114;
FAX: (202) 401-1931.

Improvement of Cereal Quality by Genetic Engineering

A symposium reviewing the potential for the application of genetic engineering to the improvement of cereal grain quality.

September 12-16, 1993

Preliminary Program

- ☐ Improvement of Cereal Protein Quality by Genetic Engineering
- ☐ Progress Towards Genetic Engineering of Wheat with Improved Quality
- ☐ An Assessment of Methods for the Genetic Transformation of Wheat
- ☐ Genetic Engineering of Rice
- ☐ Genetic Engineering of Barley
- ☐ Progress in Wheat Transformation
- ☐ Prospects for the Production of Cereals with Improved Starch Properties
- ☐ Progress in Barley and Maize Transformation
- ☐ Improvement of the Malting Quality of Barley by Genetic Engineering
- ☐ Genetic Engineering of Sorghum
- ☐ Genetic Engineering of Oats
- ☐ Development of Promoter Systems for the Tissue Specific Expression of Foreign genes in Transgenic Cereals
- ☐ Regulation of the use of Products of Genetic Engineering



43rd Australian Cereal Chemistry Conference
Holiday Inn, Coogee Beach
Sydney, Australia

For further information on Symposium program contact:

Dr. R. Henry
Vice-Chairman Cereal Chemistry
Division RACI
Queensland Agricultural
Biotechnology Centre
Gehrmann Laboratories
University of Queensland 4067
Australia
Telephone: (07) 3654962
Fax: (07) 3654980

To register contact:

Mr. W. Sing
Conference Secretary
Prime Wheat Association
P. O. Box 146
Narrabri NSW 2390
Australia
Telephone: (067) 921433
Fax: (067) 923852

Introducing Dr. Ed Coe

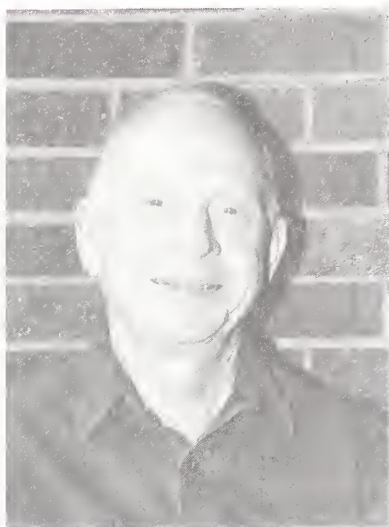


Photo by Brian Norris

Dr. Edward (Ed) Coe is a USDA Agricultural Research Service Research Geneticist and Professor of Agronomy at the University of Missouri in Columbia. He has served with USDA at the University for over 37 years.

Dr. Coe works in the Plant Genetics Research Unit where his responsibilities include conducting and supervising research on the genetic mechanisms of maize, the genetic control of plant development, and on homologous genetic systems in plant species. He also nurtures cooperative research efforts on higher plant genetics.

In addition, Dr. Coe is participating in USDA's Plant Genome Research Program efforts to develop and implement a plant genome database system. As chairman of the maize database project, he has been primarily responsible for directing

and coordinating the maize database development.

In 1992, Dr. Coe was recipient of the prestigious Thomas Hunt Morgan Medal awarded by the Genetics Society of America. The award was presented to him in recognition of the importance of his basic research, his mentorship of students and postdocs, and his extensive and outstanding service to the maize genetics community. Dr. Coe was described as "the glue that holds the maize community together."

During his career, Dr. Coe has authored and co-authored numerous publications. Since 1975, he has served as editor of the Maize Genetics Cooperation News Letter. For several years, he served as a panel member for genetic mechanisms for USDA's Competitive Grants Program. He is a member of various professional organizations, including the Genetics Society of America, the American Genetic Association, and the Crop Science Society of America.

Prior to coming to Columbia, Dr. Coe was a research fellow in biological sciences at the California Institute of Technology, Pasadena. He earned a Ph.D. in botany at the University of Illinois, and received his M.S. degree in plant genetics and a B.S. degree in agronomy and plant genetics from the University of Minnesota. ♦

Soybase Newsletter launched



The first issue of the *Soybase* newsletter was released this spring. The newsletter focuses on Soybase, the USDA Plant Genome Research Program soybean database. Regular features will include:

Update: listings of new data added to Soybase or the Soybean Gopher database.

Bug Report: sightings and fixes of software bugs.

Question and Answer: questions asked of electronic discussion groups and their answers.

Special Report: one topic, discussed in depth. The first issue of Soybase featured XWindow software.

Subscribe by writing to Lisa Lorenzen, G313 Agronomy, Iowa State University, Ames, Iowa 50011, USA, or send an Internet message to "curator@mendel.agron.iastate.edu"

A Celebration of the Life of Dr. Barbara McClintock

Renowned Geneticist Remembered at Memorial Service

*Dr. Thomas Peterson
Senior Staff Investigator
Cold Spring Harbor Laboratory
Cold Spring Harbor, NY*

At a recent memorial service to celebrate the life of distinguished geneticist and Nobel laureate Dr. Barbara McClintock, friends and colleagues reminisced about her life and outstanding achievements.

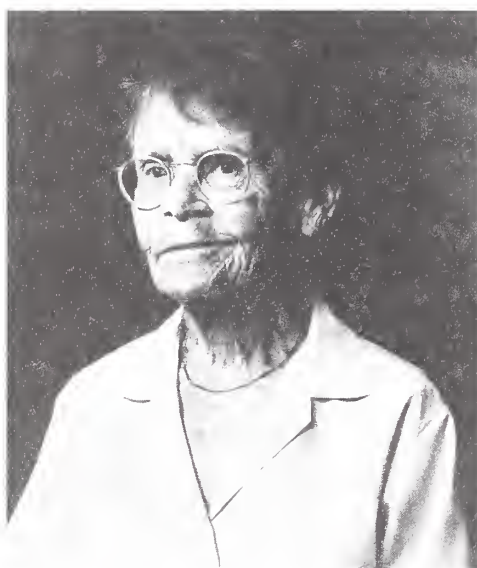
Speakers at the service, held November 17, 1992, at Cold Spring Harbor Laboratory in New York, included Howard Green (Harvard Medical School), James Shapiro (University of Chicago), Evelyn Witkin (Rutgers University), V. Sundaesan (Cold Spring Harbor Laboratory), and Oliver Nelson (University of Wisconsin, Madison).

Recognition

Howard Green noted that McClintock's early achievements in maize cytogenetics brought considerable recognition, including election to the National Academy of Sciences (1944) and election to President of the Genetics Society of America (1945). However, McClintock's reports of transposable genetic elements were not readily accepted by her scientific peers until her genetic insights were verified by molecular biologists in the 1970's.

McClintock was recipient of

several major awards, including the National Medal of Science (1970), Lasker Prize (1981), MacArthur Foundation Award (1981), and an



Photography provided by Cold Spring Harbor Laboratories Archives

unshared Nobel Prize (1983). Green commented that McClintock bore these honors with a martyr's resignation, as she was well aware of the impact the attendant publicity would have on her scientific lifestyle.

Green said McClintock never considered science as a career-- instead, she was a prototypic non-

careerist. McClintock was interested in a variety of vocations. While working in Missouri, she spent many hours at the local weather bureau.

She later indicated that if she had not entered science, she would have pursued meteorology. Green noted that McClintock did not believe that graduate students should be coddled. "Let them sink or swim!" was her motto.

Contributions

James Shapiro (University of Chicago) summarized McClintock's contributions in several areas. In the area of genome structure, McClintock likened the genome to a sophisticated erector set (although she had an intense dislike for models), whose activities were regulated by controlling elements (her term for transposable elements). Although she did not agree with certain evolutionary tenets, she believed that "any organism can make any other." One suspects that this view was sparked by observations of certain maize mutations (e.g., Corngrass), which radically alter the plant's appearance. McClintock's view has been confirmed by recent

findings of protein domains whose structure and function have been conserved among widely diverged organisms (e.g., "Myb"-type DNA binding domains of transcriptional regulatory proteins in plants, animals, and fungi).

Shapiro also stated that in the area of cellular information processing, McClintock wondered how plant cells sense the presence of broken chromosomes and activate the appropriate repair mechanisms, and she marveled at the "smart cells" that underwent specific migrations in animal embryogenesis. McClintock was known to ask seminar speakers, "How does it all fit together?" She considered reductionism as an approach, not an answer. Shapiro believed that the secret of McClintock's success, in the face of incomprehension and prejudice, was her fearless and complete intellectual freedom--to admit "I don't know," and then to wrestle the answer from the data.

Humor Noted

Evelyn Witkin (Rutgers University) treated the audience to a fresh look at McClintock's humor. After receiving the Nobel Prize, McClintock received an invitation from Henry Kissinger to a dinner for Nobel laureates. While the invitation listed all the other guests as "Dr. so and so," Barbara was referred to as "Ms. B. McClintock." McClintock penned in the margin a line from comedian Rodney Dangerfield: "I don't get no respect!"

Approachable

V. Sundaresan (Cold Spring Harbor Laboratory) spoke from the perspective of younger scientists who were receiving their Ph.D.'s when McClintock won the Nobel. Sundaresan noted that visitors to Cold Spring Harbor Laboratory regarded McClintock with awe, and wondered whether it was safe to approach her. In fact, McClintock would talk with anyone as long as the person was sincere and not just there to say he or she had met her.

Sundaresan noted that discussions with McClintock were likely to take some time--if you asked her a question, you had better be prepared to confer for a whole afternoon. According to Sundaresan, after several hours of intense dialogue, she would look closely at you and say, "We'd better stop now--you look tired!" Several days or even weeks following a session with her, one might suddenly realize the significance of something she had said that, at the time, seemed incomprehensible or irrelevant. Sundaresan emphasized that although McClintock had the reputation of a mystic, she always drew her conclusions from her observations--this is what she meant when she admonished us to "listen to the plant."

Premier Cytogeneticist

Oliver Nelson (University of Wisconsin, Madison) observed much of McClintock's progress during his own lengthy career in maize genetics. Nelson noted that she was the Nation's premier cytogeneticist, using the best organism--maize!

Nelson recalled how McClintock's first reports of transposable elements were often met with skepticism. However, Nelson's colleague and mentor, Alexander Brink, quickly recognized that McClintock's transposable elements could explain his own observations on variegated pericarp in maize. With her help, Brink and his student demonstrated that McClintock's Ac transposable element was involved in the classic pericarp variegation, which had been first studied by R.A. Emerson--the grand father of maize genetics and McClintock's own supervisor while she was a graduate student at Cornell.

Nelson concluded by noting that researchers are occasionally presented with bizarre results. McClintock possessed a special talent for recognizing the underlying order and providing an explanation for the most perplexing observations.

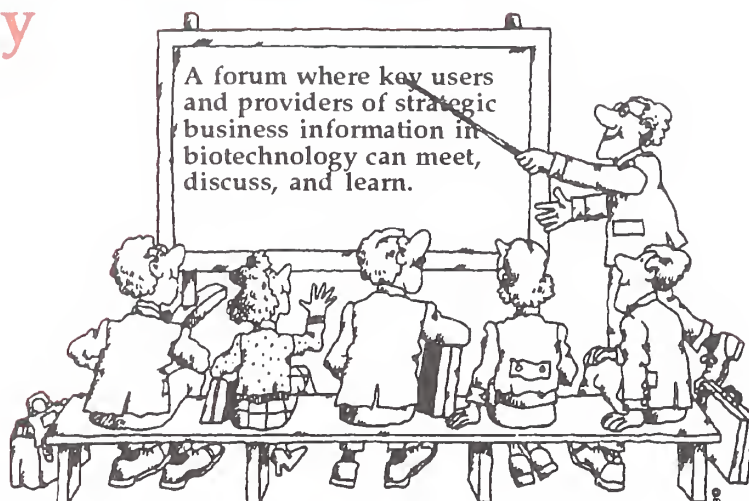
Following the scheduled speakers, Tom Brokaw, Jo Messing, and W. Szybalski added their own reminiscences. Far from a somber memorial service, this upbeat event brought McClintock's friends together to share their fond memories of an extraordinary colleague. ♦



International Conference on Strategic Business Information in Biotechnology

Registration Fee: \$299

Dates: October 11-12, 1993



Organizing Committee (and conference participants):

- ✦ Mark D. Dibner, Ph.D., conference chair, director, Institute for Biotechnology Information
- ✦ Anita Crafts-Lighty, Ph.D., director, BioCommerce Data, U.K.
- ✦ Michael Gelinne, information manager, Glaxo Research Institute
- ✦ Kenneth B. Lee, Jr., national director, Life Sciences Practice, Ernst and Young
- ✦ Rolf D. Schmid, director, biotechnology program, GBF Braunschweig, Germany
- ✦ Susan McCarthy, Ph.D., coordinator, Plant Genome Data and Information Center, U.S.D.A.
- ✦ Nancy G. Bruce, librarian, Institute of Biotechnology Information
- ✦ Kevin O'Connor, BioApplications Program, U.S. Office of Technology Assessment
- ✦ Bernard Zechendorf, documentalist, EEC BIODOC Program, Belgium
- ✦ Other speakers to be announced

Place: Conference and Education Facility, North Carolina Biotechnology Center
Triangle Park, North Carolina, U.S.A.

For further information contact:

Institute for Biotechnology Information, North Carolina Biotechnology Center, P.O. Box 13547, Research Triangle Park, NC 27514-3547 Telephone: (919)549-8880 Fax: (919)990-9521

Genome Conservation Highlighted at Plant Genome I Conference.

*Dr. Susan McCarthy, Coordinator
USDA/National Agricultural Library
Plant Genome Data & Information Center
Beltsville, MD*

Genome organization is remarkably conserved between related species, reported participants at the recent Plant Genome I Conference, Nov. 9-11, 1992, in San Diego, CA. The meeting was co-sponsored by the USDA / ARS Plant Genome Research Program. Over 400 participants from around the world came together to share their research findings, with the belief that understanding genome conservation and organization should lead to faster and more efficient mapping across many species.

Conservation.

Conservation was observed primarily in the low copy DNA segments, while variability, including highly repetitive sequences, were found in flanking regions. These observations were made by a number of researchers, including Jeff Bennetzen (Purdue University, West Lafayette, IN), who found that low-copy sorghum sequences conserved in maize were also largely colinear. A similar finding was made by Steve Tanksley (Cornell University, Ithaca, NY) for maize and rice; 70% of single copy DNA was conserved and whole chromosome or chromosomal arms had maintained the same gene order.

Wheat and barley are largely syntenic, that is, the linear gene order is maintained along the chromosomes. Graham Moore (Cambridge Laboratory, Norwich, U.K.) observed 60% cross-hybridization of rice and wheat markers, and that copy numbers were also conserved in the low

copy number segments. See Table 1 for a summary.

Data Management.

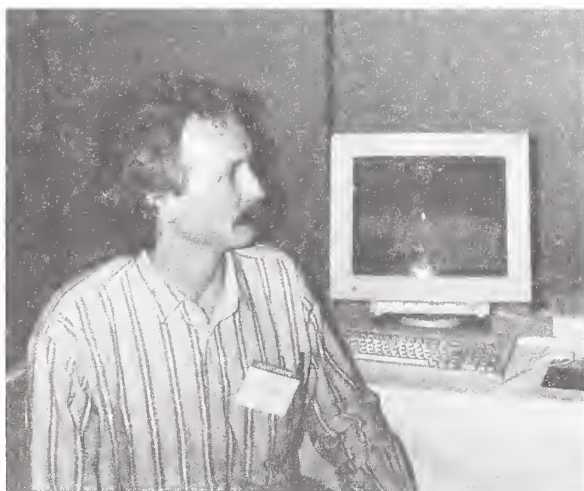
These exciting findings point to the need for data management. Tools for storing and analyzing data were discussed throughout the meeting. A mapping software workshop spon-

Table 1 - Some Observations from Plant Genome I

Investigator	Species	Observations
J. Bennetzen	sorghum / maize	Low copy sequences: cross hybridize; same number
M. Gale	wheat / rye	Maps very similar: 7 translocations, 11 break-points found
J. Gustafson G. Moore	wheat / rye / barley / rice	Considerable synteny for cereals in RFLP maps
G. Moore	wheat / rice	Markers cross-hybridize; significant micro-synteny
A. D'Hont	maize / sugarcane	High degree of synteny
G. King	Brassica / Arabidopsis	85% conservation of homologous exons
M. Lee	Sorghum / maize	80% of linked sorghum markers were also linked in maize.
N. Weeden	pea / lentil / chickpea	Significant conservation but not as high as maize / rice
S. Tanksley	tomato / potato / pepper	5 chromosomal inversions distinguish potato - tomato
S. Tanksley	maize / wheat / rice	Rice chromosome 4 like wheat chromosomes 2 and maize 2S without major rearrangements
S. Tanksley	maize / rice	70% rice single copy cDNA conserved in maize; synteny retained for whole and partial chromosomes

sored by Ed Coe (University of Missouri, Columbia, MO), Mary Berlyn (Yale University, New Haven, CT), and Stan Letovsky (Letovsky Associates, New Haven, CT) attracted a standing-room-only crowd of about 200 scientists. Software developments, capabilities, and needs were presented for MapMaker, GMendel, JoinMap, CProp, Hypergene, and others. Steve Knapp (GMendel: Oregon State University, Corvallis, OR) and Steve Lincoln (MapMaker: Massachusetts Institute of Technology, Cambridge, MA) have agreed to cooperate more fully in future software developments.

The Plant Genome Database,



Mike Cherry (shown above) and Brad Sherman organized the database demonstrations at Plant Genome I.



Dr. Rose Broome and assistant Pam Mitchell demonstrated the Plant Genome database.

Map-Based Breeding.

The end product of genome mapping is map-based breeding and gene isolation. Steve Tanksley gave an elegant demonstration of map-based breeding in tomato. The process is as follows: wild-type tomatoes which did not exhibit desirable phenotypic traits were bred. A high-density molecular marker map was then used to eliminate such undesirable

traits as small fruits or poor taste quality. The end result was a tomato that grew 15% faster and had a 15% greater yield than standard varieties.

Marker-assisted selections are especially important for long-life-cycle species, including trees. Some marker-assisted selections are now being used, in apple tree breeding, for example. A Forest Tree Genome Mapping Workshop, organized by David Neale (U.S. Forest Service, Albany, CA), was held in conjunction with the Plant Genome I conference (see the report on page 4). ♦

central database of the Plant Genome Research Program, was demonstrated, as were all of the species-specific sub-databases. Dave Kristofferson (Intelligenetics, Inc., Mountain View, CA) organized an informal workshop to look at electronic communications for Plant Biologists with the BioSci Newsgroups.

Plant Genome I in the news:

Dutton, G. (1992) Plant species gene maps yield surprises. *Genetic Engineering News* 12(19):1,3,37.

Havukkala, I. (1992) Plant Genome I meeting highlights. *Rice Genome* 1(2):15.

Announcing PLANT GENOME II

An International Conference
on the Plant Genome

January 24-27, 1994
Town & Country Hotel
San Diego, CA

Sponsors

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M. Gale, John Innes Centre, Norwich, UK

J. Miksche, USDA/ARS, Beltsville, MD
K. Takayanagi, University of Tsukuba, Japan

Organizer

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11 Penn Plaza, Suite 1003, New York, NY 10001, Tel: (212) 643-1750, Fax: (212) 643-1758
e-mail: PGENOME@NALUSDA.GOV

**Participants are invited to submit abstracts for the poster session.
Abstract deadline for inclusion in the Final program is November 15, 1993**

- ☐ Please send registration information.
☐ Please send abstract form.
☐ Please send information on exhibiting.

Plant Genome II

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Plant Genome Publications

The following publications are available. If you would like to receive a copy, check off the title and mail your request to:

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Quick Bibliographies:

The AGRICOLA bibliographic database was searched by topic. A bibliography was compiled of the relevant citations; abstracts are included when available.

Biotechnology: Genetic Engineering for Crop Plant Improvement. January 1991 - March 1992. 320 citations. 102 pp. Prepared by Robert D. Warmbrodt and Lara Wiggert. QB 92-48

Biotechnology: Genetic Linkage Studies (Gene Mapping) in Plant Systems. January 1989 - March 1991. 433 citations, 59 pp. Prepared by Robert D. Warmbrodt. QB 91-114

Biotechnology: Plant Protection from Nonviral Agents. January 1991 - December 1992. 306 citations, 63

pp. Prepared by Daniel Cabirac and Robert D. Warmbrodt. QB 93-13

Breeding and Selecting Crops for Insect Pest Resistance. January 1986 - December 1991. 496 citations. 117 pp. Prepared by Jane Potter Gates. QB 92-25

Gene Expression in Field Crops. January 1991 - November 1991. 258 citations. 117 pp. Prepared by Janet Saunders and Robert D. Warmbrodt. QB 93-16

Gene Expression in Horticultural Crops. January 1991 - October 1992. 215 citations. 93 pp. Prepared by Robert D. Warmbrodt and Janet Saunders. QB 93-08

Miscellaneous Publications:

Prepared by the Biotechnology Information Center staff.

Databases Pertaining to Biotechnology.

Biotechnology Directories

Guide to Information Sources in Biotechnology

Newsletters Pertaining to Agricultural Biotechnology

ALF (Agricultural Library Forum): The National Agricultural Library's Electronic Bulletin Board System - Brief Guide. Prepared by Karl Schneider



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